

MAR. -22' 04 (MON) 18:16

ALSTON & BIRD

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P. 027

In re: Mahajan et al..
Appl. No. 09/954,950
Filed September 18, 2001

APPENDIX TAB 3

GAP of: 1285AP003238MLH1aa check: 4284 from: 1 to: 715

WPDEF Case 1285 Rice MLH1 protein encoded by genomic cda from GenBank
AP003238

Rice chromosome 1

Case 1285 Rice MLH1 protein encoded by genomic cda from GenBank
AP003238 Rice

chromosome 1

ANNOTATED AS MLH1 4/13/02.

Join(33330 .33566,33690 .33862,33943 .34015,34105 .34239, . . .

to: 1285sid2 check: 8164 from: 1 to: 724

WPDEF Case 1285 MLH-1 SEQ ID NO:2 O. sativa

Case 1285 MLH-1 SEQ ID NO:2 O. sativa

Symbol comparison table: blosum62.cmp CompCheck: 1102

BLOSUM62 amino acid substitution matrix.

Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
substitution matrices from protein blocks. Proc. Natl.
Acad.

Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
Length Weight: 2 Average Mismatch: -2.248

Quality: 3639 Length: 725
Ratio: 5.090 Gaps: 1
Percent Similarity: 99.860 Percent Identity: 99.860

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

1285AP003238MLH1aa x 1285sid2 March 9, 2004 15:35 ..

```
1 MDEPSPRQGGCAGEPPRIRRLRESVNNRIAAGEVIQRPSSAVKELIENSL 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 MDEPSPRQGGCAGEPPRIRRLRESVNNRIAAGEVIQRPSSAVKELIENSL 50

51 DAGASSVSVAVKDGGLKLIQVSDDGHGIRFEDLAILCERHTTSKLSAYED 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 DAGASSVSVAVKDGGLKLIQVSDDGHGIRFEDLAILCERHTTSKLSAYED 100

101 LQTIKSMGFRGEALASMTYVGHVTVTTITBQLHGQYRVSYRDQVMENEPK 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 LQTIKSMGFRGEALASMTYVGHVTVTTITBQLHGQYRVSYRDQVMENEPK 150

151 PCAAVKQTOVMVENLFYNMVARKKTLQNSNDDYPKIVDFISRFVHHINV 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 PCAAVKQTOVMVENLFYNMVARKKTLQNSNDDYPKIVDFISRFVHHINV 200

201 TFSCRKHGANRADVHSASTSSRLDAIRSVYGASVVRDLIEIKVSYEDAAD 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 TFSCRKHGANRADVHSASTSSRLDAIRSVYGASVVRDLIEIKVSYEDAAD 250
```

251 SIFKMDGYISNANYVAKKITMILFINDRLVDCTALKRAIEFVYSATLPQA 300
|||||
251 SIFKMDGYISNANYVAKKITMILFINDRLVDCTALKRAIEFVYSATLPQA 300
301 SKPFTYMSIHLPSHVVDVNIHPTKKEVSLNQERIETIRNAIEEKLMS 350
|||||
301 SKPFTYMSIHLPSHVVDVNIHPTKKEVSLNQERIETIRNAIEEKLMS 350
351 NTTRIFQTQALNLSGIAQANPQKDKVSEASMOSGTSQKIPVSQMVRTDP 400
|||||
351 NTTRIFQTQALNLSGIAQANPQKDKVSEASMOSGTSQKIPVSQMVRTDP 400
401 RNPSGRLHTYWHGQSSNLEKKFDLVSVRNVVRSRRNQKQAGDLSSRHELL 450
|||||
401 RNPSGRLHTYWHGQSSNLEKKFDLVSVRNVVRSRRNQKQAGDLSSRHELL 450
451 VEIDSSFPGLLDIVKNCTYVGLADEAFALIQHNTRLVNVVNISKELM 500
|||||
451 VEIDSSFPGLLDIVKNCTYVGLADEAFALIQHNTRLVNVVNISKELM 500
501 YQQALCRFGNFNAIQLSEPAPLQELLVMALKDDELMSDEKDEKLEIAEV 550
|||||
501 YQQALCRFGNFNAIQLSEPAPLQELLVMALKDDELMSDEKDEKLEIAEV 550
551 NTEILKENAEMINBYFSIHIDQDGKLTRLPVVLDQYTPDMDRLPEFVLAL 600
|||||
551 NTEILKENAEMINBYFSIHIDQDGKLTRLPVVLDQYTPDMDRLPEFVLAL 600
601 QNDVTWDDKEKCFRTVASAVGNFYALHFPILPNPSONGIHLYKKNRDSMA 650
|||||
601 QNDVTWDDKEKCFRTVASAVGNFYALHFPILPNPSONGIHLYKKNRDSMA 650
651 DEHAENDLISDENDVPQELLAEFAAWAQREWTIQHVLFPMSRLFLKPPK 700
|||||
651 DEHAENDLISDENDVPQELLAEFAAWAQREWTIQHVLFPMSRLFLKPPK 700
701 SMATDGTFFVQVPSDL..... 715
|||||
701 SMATDGTFFVQVAS.LEKLYKIFERC 724

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APPENDIX TAB 4